Package ‘FeatSeekR’

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Type Package

Title FeatSeekR an R package for unsupervised feature selection

Version 1.4.0

Description FeatSeekR performs unsupervised feature selection using replicated measurements. It iteratively selects features with the highest reproducibility across replicates, after projecting out those dimensions from the data that are spanned by the previously selected features. The selected a set of features has a high replicate reproducibility and a high degree of uniqueness.

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Encoding UTF-8

Imports pheatmap, MASS, pracma, stats, SummarizedExperiment, methods

RoxygenNote 7.2.3

Suggests rmarkdown, knitr, BiocStyle, DmelSGI, testthat (>= 3.0.0)

VignetteBuilder knitr

BugReports https://github.com/tcapraz/FeatSeekR/issues

URL https://github.com/tcapraz/FeatSeekR

biocViews Software, StatisticalMethod, FeatureExtraction, MassSpectrometry

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**calcFstat**

**Description**

calcFstat

**Usage**

calcFstat(data, fac)

**Arguments**

data 2 dimensional array with samples x features, where samples belongs different conditions. The function was adapted from the genefilter package.

fac factor of length samples, indicating which sample belongs to which condition

**Value**

F-statistic for all features

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**check_input**

**Description**

Checks input data. Input data should be a 2 dimensional array with features x samples or SummarizedExperiment carrying one assay named data and colData indicating which sample belongs to which condition
Usage

check_input(data, max_features, conditions = NULL)

Arguments

data input data provided toFeatSeek either SummarizedExperiment or 2 dimensional array with features x samples
conditions if data is a 2 dimensional array with features x samples a factor indicating which sample corresponds to which condition must be provided

Value

SummarizedExperiment where condition information is stored in colData

Description

This function ranks features of a 2 dimensional array according to their reproducibility between conditions.

Usage

FeatSeek(
  data,
  conditions = NULL,
  max_features = NULL,
  init = NULL,
  verbose = TRUE
)

Arguments

data SummarizedExperiment with assay named data, where samples belongs to different conditions. Which sample belongs to which condition should be indicated in colData slot conditions. Or matrix with features x samples. Each conditions have multiple samples from replicated measurements.
conditions factor of length samples, indicating which sample belongs to which condition. Only required if data is provided as matrix.
max_features integer number of features to rank
init character vector with names of initial features. If NULL the feature with highest F-statistic will be used
verbose logical indicating whether messages should be printed
Value

SummarizedExperiment containing one assay with the selected features. rowData stores for each selected feature the F-statistic under metric, the cumulative explained variance under explained_variance and the feature names under selected

Examples

# run FeatSeek to select the top 20 features
data <- array(rnorm(100*30), dim=c(30, 100),
dimnames <- list(paste("feature", seq_len(30)), NULL))
conds <- rep(seq_len(50), 2)
res <- FeatSeek(data, conds, max_features=20)

# res stores the 20 selected features ranked by their replicate
# reproducibility
Description

Fit linear model for each feature as a function of the previously selected features $S$. The dimensions spanned by the selected features are projected out of the data by setting each feature to its residuals from the linear model fit.

Usage

$\text{fit\_lm(data, } S, k)$

Arguments

data : data (2 dimensional array samples x features)
S : set of selected features
k : current iteration

Value

data with previously selected features projected out

Description

Checks if preselected init features are in input data. If init is NULL, it is set to feature with highest condition correlation.

Usage

$\text{init\_selected(init, se)}$

Arguments

init : preselected starting set of features
data : input data as SummarizedExperiment

Value

names of initial set of feature
plotSelectedFeatures

Description

plot correlation matrix of selected feature sets

Usage

plotSelectedFeatures(res, n_features = NULL, assay = "selected")

Arguments

res      result SummarizedExperiment from FeatSeek function
n_features top n_features to plot. if NULL then the maximum number of features in res will be plotted
assay    assay slot to plot from result SummarizedExperiment object, default is the selected features slot

Value

returns heatmap of selected features

Examples

# run FeatSeek to select the top 20 features
data <- array(rnorm(100*30), dim=c(30,100),
              dimnames = list(paste("feature", seq_len(30)), NULL))
conds <- rep(seq_len(50), 2)
res <- FeatSeek(data, conds, max_features=20)

# res stores the 20 selected features ranked by their replicate
# reproducibility
# plot the top 5 features
plotSelectedFeatures(res, n_features=5)

plotVarianceExplained

Description

plot variance explained from 1 to max_features in res

Usage

plotVarianceExplained(res)
Arguments

- `res`: result `SummarizedExperiment` from `FeatSeek` function

Value

returns plot of variance explained vs number of features

Examples

```r
# run FeatSeek to select the top 20 features
data <- array(rnorm(100*30), dim=c(30,100),
             dimnames = list(paste("feature", seq_len(30)), NULL))
conds <- rep(seq_len(50), 2)
res <- FeatSeek(data, conds, max_features=20)

# res stores the 20 selected features ranked by their replicate
# reproducibility
plotVarianceExplained(res)
```

Description

simulate Data with orthogonal feature clusters and replicated samples. Each feature cluster corresponds to a different latent factor and contains 10 redundant features. E.g. choosing `samples = 100`, `n_latent_factors = 5` and `replicates = 2` will simulate a 50 x 200 data matrix, where the first 100 samples belong to replicate 1 and sample 101-200 belong to replicate 2.

Usage

`simData(conditions, n_latent_factors, replicates)`

Arguments

- `conditions`: number of conditions to generate samples from
- `n_latent_factors`: number of latent factors to generate
- `replicates`: number of replicates to generate

Details

`simData` constructs `n_latent_factors` by generating a random matrix `Q` whose row vectors `Q_i \sim \mathcal{N}(0, 1)` with `n` samples and `i \in \{1, \ldots, n\_latent\_factors\}` are orthonormal, each corresponding to a different latent factor. To simulate a set of redundant feature groups, it generates 10 features `X_j` for each latent factor `Q_i` by scaling each latent factor by a random factor `\delta_j \sim \mathcal{N}(0, 1)` and adding replicate specific noise `\epsilon_{c} \sim \mathcal{N}(0, 0.1)` with `c \in \{1, \ldots, replicates\}` preserving orthogonality.
Value

SummarizedExperiment object carrying simulated data, with colData indicating which sample belongs to which replicate

Examples

# simulate data 100 samples from 100 conditions, 20 features generated by 2 # latent factors and 2 replicates
simData(conditions=100, n_latent_factors=2, replicates=2)

<table>
<thead>
<tr>
<th>variance_explained</th>
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</tr>
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</table>

Description

variance_explained

Usage

variance_explained(data, selected)

Arguments

data 2 dimensional array samples x features
selected character vector of selected features

Value

average variance explained by selected features
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